REPORT DOCUMENTATION PAGE

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Approved for public release; distribution is unlimited.

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The views, opinions and/or findings contained in this report are those of the author(s) and should not contrued as an official Department of the Army position, policy or decision, unless so designated by other documentation.

14. ABSTRACT

15. SUBJECT TERMS

16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT	15. NUMBER OF PAGES	19a. NAME OF RESPONSIBLE PERSON
a. REPORT	b. ABSTRACT	c. THIS PAGE			Melik Demirel
UU	UU	UU	UU		19b. TELEPHONE NUMBER 814-863-2270

RPPR Final Report
as of 30-Jan-2019

Agency Code:

Proposal Number: 70006LSRIP **Agreement Number: W911NF-17-1-0155**
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DUNS Number: 003403953 EIN: 246000376

Report Date: 13-Jul-2018 Date Received: 08-Oct-2018
Final Report for Period Beginning 14-Apr-2017 and Ending 13-Apr-2018
Title: High-Throughput Screening of Evolutionary Biological Materials
Begin Performance Period: 14-Apr-2017 **End Performance Period:** 13-Apr-2018
Report Term: 0-Other

Submitted By: Melik Demirel Email: mcd18@psu.edu
Phone: (814) 863-2270

Distribution Statement: 1-Approved for public release; distribution is unlimited.

STEM Degrees: 0 **STEM Participants:** 2

Major Goals: The goal of this project is to establish the genetic basis of fiber forming protein structures via a pioneering high-throughput screening system based on transient thermal-reflectivity (TTR) spectroscopy. This novel method offers the first high-throughput screening tool that reports on the structural features of protein aggregation. Here, we propose to screen an ultra-large number (109) of potential fiber-forming genes. We will achieve the proposed goal by investigating three fundamental questions: (i) what is the underlying sequence-structure relationship for protein aggregation? (ii) what is the complete set of fiber-forming proteins, given that only few have been discovered up to date?; and (iii) how can we uncover new fiber-forming genes in bacterial targets? The proposed approach will generate fundamental knowledge about fiber-promoting genes. Recently, we discovered a new technique to screen protein sequences based ultrafast laser-probing spectroscopy, which has never been applied before in this research domain. Our novel TTR technique enables screening of 10^8-10^9 different structural polypeptide sequences for protein aggregates formation in hours, a feat that would be impossible to achieve with existing screening tools such as fluorescence, immunostaining, or functional assays. Successful development of this TTR-based screening approach for proteins will have a significant impact on multiple applications for DoD in various fields (e.g., materials science, agriculture, and medicine) and open new avenues of protein research.

Accomplishments: The DURIP equipment is installed at Earth and Engineering Science Bldg first floor at Room 108, which is a laboratory space available to Dr. Demirel (PI). A pdf document containing the picture of the instrument is uploaded as well.

Currently, we are working towards obtaining data for the protein library. The library project is recently funded by a three year research grant by ARO (W911NF1810261). Hence this instrument is key for the successful completion of the existing research grants.

Training Opportunities: Nothing to Report

Results Dissemination: Nothing to Report

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as of 30-Jan-2019

Honors and Awards: Nothing to Report

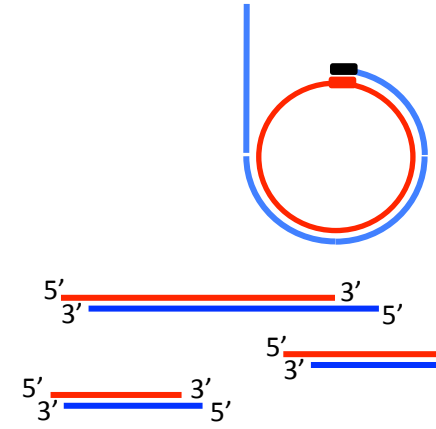
Protocol Activity Status:

Technology Transfer: Nothing to Report

PARTICIPANTS:

Participant Type: PD/PI
Participant: Melik Demirel
Person Months Worked: 3.00
Project Contribution:
International Collaboration:
International Travel:
National Academy Member: N
Other Collaborators:

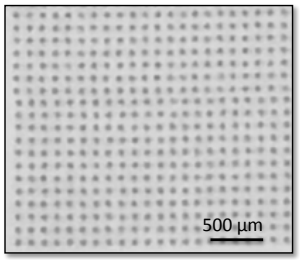
Funding Support:

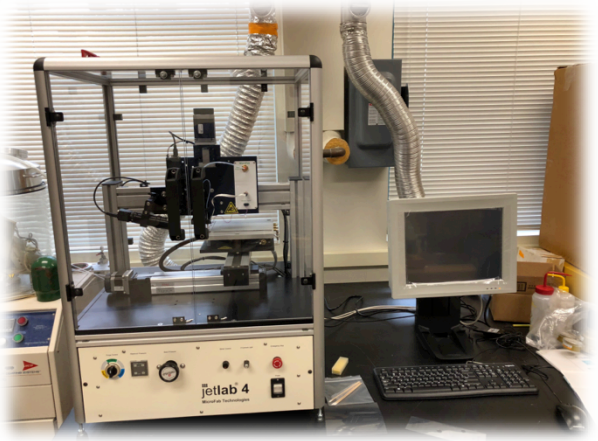


DNA Library

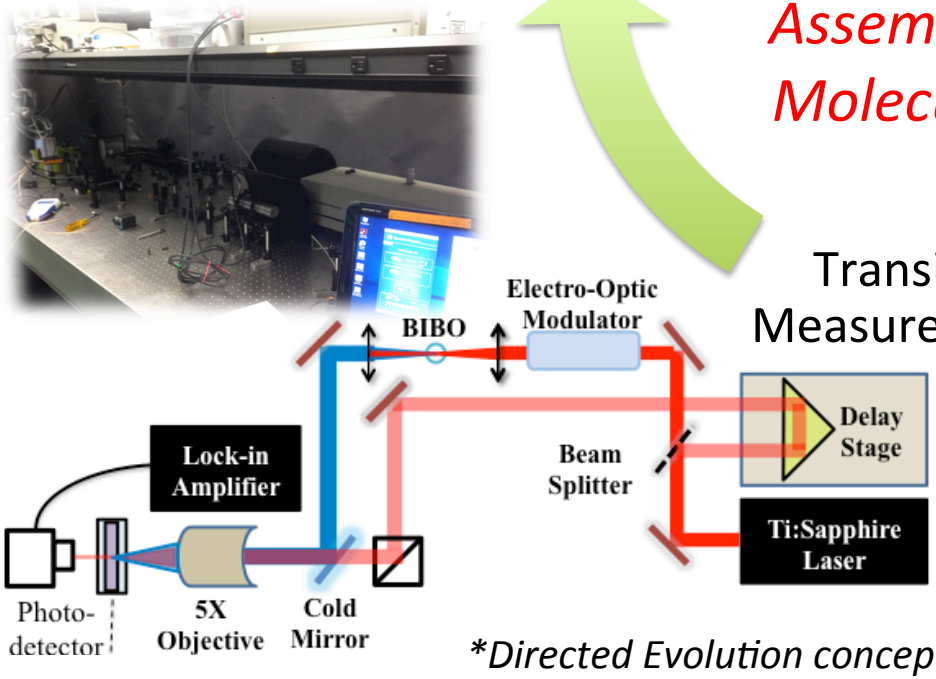
Directed Evolution of Assembler Molecules

High-throughput Array





Transient Measurements



**Directed Evolution concept received Nobel Prize 2018 in Chemistry*